

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2694	cho-y-j.in. or lee-i-s.in. or hur-j-h.in. or ahn-b-y.in. or yoo-w-i.in.	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/12/31 15:25
L2	1	L1 and (BMP-7 or BMP7 or OP-1 or OP1)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/12/31 15:26
S7	1	"20010003126" and scar and corneal	US-PGPUB; USPAT	OR	ON	2007/12/28 22:45
S8	1	("200220077270" or "20020042473") and scar and corneal and (dosage or amount or dose)	US-PGPUB; USPAT	OR	ON	2007/12/28 16:32
S16	196	(BMP-7 or BMP7 or OP-1 or OP1) same (ng/ml or ug/ml or ng/kg or ug/kg)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/12/31 15:26
S17	140	S16 and @ay<="2003"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/12/30 22:55
S19	6	S17 and (scar or (wound adj healing)) and corneal	US-PGPUB; USPAT	OR	ON	2007/12/28 22:46
S20	59	(BMP-7 or BMP7 or OP-1 or OP1) same (pro-domain or propeptide)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/12/30 22:55

EAST Search History

S21	38	S20 and (ng/ml or ug/ml or ng/kg or ug/kg)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/12/30 22:55
S22	20	S21 and @ay<="2003"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/12/31 15:24

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(FILE 'HOME' ENTERED AT 15:54:12 ON 31 DEC 2007)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS, PCTFULL' ENTERED AT 15:54:29 ON 31
DEC 2007

L1 0 S (BMP-7 OR BMP7 OR OP-1 OR OP1) (S) (NG/ML OR UG/ML OR NG/KG O
L2 680 S (BMP-7 OR BMP7 OR OP-1 OR OP1) (S) (PG OR NG OR UG OR MG)
L3 14 S L2 AND (SCAR OR (WOUND HEAL?)) AND CORNEA?
L4 5 S L3 AND PY<=2003
L5 5 DUP REM L4 (0 DUPLICATES REMOVED)
L6 1345 S CHO Y J/AU OR LEE I S/AU OR HUR J H/AU OR AHN B Y/AU OR YOO W
L7 0 S L6 AND (BMP-7 OR BMP7 OR OP-1 OR OP1)

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<!--StartFragment-->RESULT 3
BMP7_HUMAN
ID   BMP7_HUMAN      STANDARD;          PRT;   431 AA.
AC   P18075; Q9H512; Q9NTQ7;
DT   01-NOV-1990, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1990, sequence version 1.
DT   25-JUL-2006, entry version 78.
DE   Bone morphogenetic protein 7 precursor (BMP-7) (Osteogenic protein 1)
DE   (OP-1) (Eptotermin alfa).
GN   Name=BMP7; Synonyms=OP1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.
RC   TISSUE=Placenta;
RX   MEDLINE=90291971; PubMed=2357959;
RA   Oezkaynak E., Rueger D.C., Drier E.A., Corbett C., Ridge R.J.,
RA   Sampath T.K., Oppermann H.;
RT   "OP-1 cDNA encodes an osteogenic protein in the TGF-beta family.";
RL   EMBO J. 9:2085-2093(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=91088608; PubMed=2263636;
RA   Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
RA   Wang E.A., Wozney J.M.;
RT   "Identification of transforming growth factor beta family members
RT   present in bone-inductive protein purified from bovine bone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA   Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaeslaiho M.H., Lerversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Utsdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP INTERACTION WITH SOSTDC1.
 RX PubMed=15020244; DOI=10.1016/j.bbrc.2004.02.075;
 RA Yanagita M., Oka M., Watabe T., Iguchi H., Niida A., Takahashi S.,
 RA Akiyama T., Miyazono K., Yanagisawa M., Sakurai T.;
 RT "USAG-1: a bone morphogenetic protein antagonist abundantly expressed
 RT in the kidney.";
 RL Biochem. Biophys. Res. Commun. 316:490-500(2004).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 293-431.
 RX MEDLINE=96149402; PubMed=8570652; DOI=10.1073/pnas.93.2.878;
 RA Griffith D.L., Keck P.C., Sampath T.K., Rueger D.C., Carlson W.D.;
 RT "Three-dimensional structure of recombinant human osteogenic protein
 RT 1: structural paradigm for the transforming growth factor beta
 RT superfamily.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:878-883(1996).
 CC -!- FUNCTION: Induces cartilage and bone formation. May be the
 CC osteoinductive factor responsible for the phenomenon of epithelial
 CC osteogenesis. Plays a role in calcium regulation and bone
 CC homeostasis.
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with SOSTDC1.
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- TISSUE SPECIFICITY: Expressed in the kidneys and bladder. Lower
 CC levels seen in the brain.
 CC -!- PHARMACEUTICAL: Available under the names Osigraft (Stryker). Its
 CC use is indicated in the treatment of tibial non-union of at least
 CC 9 month duration, secondary to trauma, in skeletally mature
 CC patients, in cases where autograft has failed or is unfeasible.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; X51801; CAA36100.1; -; mRNA.
 DR EMBL; M60316; AAA36738.1; -; mRNA.
 DR EMBL; AL122058; CAB90273.2; -; Genomic_DNA.
 DR EMBL; AL157414; CAB90273.2; JOINED; Genomic_DNA.
 DR EMBL; AL157414; CAC08434.2; -; Genomic_DNA.
 DR EMBL; AL122058; CAC08434.2; JOINED; Genomic_DNA.
 DR EMBL; BC008584; AAH08584.1; -; mRNA.
 DR PIR; C39263; BMHU7.
 DR UniGene; Hs.473163; -.
 DR PDB; 1BMP; X-ray; @=293-431.
 DR PDB; 1LX5; X-ray; A=293-431.
 DR PDB; 1LXI; X-ray; A=293-431.
 DR PDB; 1M4U; X-ray; L=293-431.
 DR Ensembl; ENSG00000101144; Homo sapiens.
 DR H-InvDB; HIX0015936; -.
 DR HGNC; HGNC:1074; BMP7.
 DR MIM; 112267; gene.
 DR LinkHub; P18075; -.
 DR RZPD-ProtExp; A0309; -.
 DR RZPD-ProtExp; IOH5475; -.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF_beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW 3D-structure; Chondrogenesis; Cytokine; Developmental protein;
 KW Differentiation; Direct protein sequencing; Glycoprotein;
 KW Growth factor; Osteogenesis; Pharmaceutical; Signal.
 FT SIGNAL 1 29 Potential.
 FT PROPEP 30 292 Potential.
 FT /FTId=PRO_0000033876.

FT	CHAIN	293	431	Bone morphogenetic protein 7.
FT				/FTId=PRO_0000033877.
FT	CARBOHYD	187	187	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	302	302	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	321	321	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	372	372	N-linked (GlcNAc. . .) (Potential).
FT	DISULFID	330	396	
FT	DISULFID	359	428	
FT	DISULFID	363	430	
FT	DISULFID	395	395	Interchain.
FT	STRAND	329	333	
FT	STRAND	336	338	
FT	HELIX	339	342	
FT	TURN	343	343	
FT	TURN	345	347	
FT	STRAND	348	350	
FT	STRAND	352	355	
FT	STRAND	358	362	
FT	STRAND	365	366	
FT	HELIX	369	371	
FT	HELIX	375	386	
FT	TURN	388	390	
FT	STRAND	396	409	
FT	TURN	411	412	
FT	STRAND	413	413	
FT	STRAND	415	430	
SQ	SEQUENCE	431 AA;	49313 MW;	47A05E45C6815F8A CRC64;

Query Match 95.5%; Score 684; DB 1; Length 431;
 Best Local Similarity 96.4%; Pred. No. 3.9e-57;
 Matches 134; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	1	MHVASLRAAAPHSFVALWAPLFLRLRSALADFSLDNEVHSSFIHRRRLRSQERREMQREILS	60
Db	1	MHVRSLRAAAPHSFVALWAPLFLRLRSALADFSLDNEVHSSFIHRRRLRSQERREMQREILS	60
Qy	61	ILGLPHRPRPHLQGLHNSAPMFMLDLTNAMAVEEGGGPGGQGFSTPTKAVFSTQGPPPLAS	120
Db	61	ILGLPHRPRPHLQGLHNSAPMFMLDLTNAMAVEEGGGPGGQGFSTPYKAVFSTQGPPPLAS	120
Qy	121	LQDSHFLTDADMVMSFVNL	139
Db	121	LQDSHFLTDADMVMSFVNL	139

<!--EndFragment-->